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Microbial communities associated to rubber tree plantations along a chronosequence in North East Thailand

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Rubber tree (*Hevea brasiliensis*) is a crop of major socio-economic importance in Southern Asia as it represents a substantial source of income for small land holders. In Thailand (1/3 of world latex production) rubber tree plantations are currently greatly expanding in adverse eco-climatic zones, especially in Isan provinces, where soils have sandy texture, low fertility and are prone to erosion and leaching of applied fertilizers. A major potential for increased production in these conditions relies on the important roles of rhizosphere microbial communities in supporting soil fertility and plant nutrition. A chronosequence of 3, 6 and 16 year-old plantations was identified and cassava fields were used as no-rubber controls for comparison. Soils from each treatment were characterized for texture and chemistry. Using 454 sequencing, total bacterial and fungal communities as well as arbuscular mycorrhizal fungi (AMF) community were analyzed. Because they are known to contribute to plant P and N nutrition by increasing mineral nutrient availability or by enhancing plant nutrient uptake, root-interacting P-solubilizing bacteria (PSB) and free living N fixing bacteria were assessed after culturing on selective media. Nematodes populations were characterized as there are good soil fertility indicators. Functional traits were also analyzed by both qPCR and Ecoplates (Biolog) methods. Results showed significant differences between rubber and cassava associated communities but didn't reveal a strong impact of the age of the plantations on the different communities. For instance, the AMF community in cassava roots was twice as rich as in rubber tree samples but was not affected by the age of rubber trees. The improved understanding of the diversity of root-associated microbes will contribute to the development of alternative sustainable practices to improve and sustain soil fertility.

Keywords: Rubber tree, Microbial communities, Chronosequence, Northeast Thailand